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PROJECT 1 ABSTRACT

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Diploid *Lophopyrum elongatum*, tall wheatgrass, is highly resistant to Fusarium head blight (FHB). Previous studies, utilizing a complete set of 21 disomic substitution lines of the seven *L. elongatum* chromosomes in the Chinese Spring wheat genetic background mapped FHB resistance on the long arm of chromosome 7E. Similar findings were made with a chromosome 7e12 derived from a closely related decaploid tall wheatgrass (*L. ponticum*). The close relationships between the two tall wheatgrass taxa and the location of the resistance on the same chromosome arm suggests that the same locus, *Fhb7*, is involved. The *Fhb7* locus has been mapped in the distal region of the 7e12 chromosome. We employed our recently completed genome sequence of *Aegilops tauschii*, the source of the D genome of common wheat, and showed that the *Fhb7* region is colinear between 7D and homoeologous chromosomes in other grass genomes, making it highly probable that it is also colinear between 7D and 7E. We have developed introgression lines in which chromosome 7E is recombined with 7D. We will map FHB resistance in these lines and use them as an initial material for further recombination and development of introgression material for wheat breeding. We will also backcross existing and second-generation introgression lines into other wheat genotypes to evaluate their agronomic attributes and suitability of *Fhb7* for pyramiding with *Fhb1*. Accomplishing the objectives of this project will benefit the US wheat industry by providing it with new and exceptionally effective resistance to FHB that can be immediately deployed in wheat improvement.